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OM protein - protein search, using sw model

January 16, 2003, 16-39-12 . Search time 7-28071 Seconds (without alignments) 28-464 Million cell updates/sec Pun on:

Title:  $0S-09-856 \cdot 070-25$ Perfect score: 23Sequence: 1 MLRLQ 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues

112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ				
Result		Query				
NO.	Score	Match	Match Length	E DB	0.1	Description
		100 0	160		Y650 TREEPA	083656 treponema p
C4		100.0	196		RL19 HUMAN	8
en		100.0	244		HL51_HSVE4	ogne-
4	83	100.0	0.44 0.44 0.45	ч	UL51_HSVEB	
ĸ		100 0	288	_	PEF1_SCHPO	
ٹ		Jou o	313		PYPH_AGRIF	
7	23	100.0	313	_	PYRH_RH!ME	Q92q15 rhizobium m
œ	53		317	П	MTB1_NEIGO	Q59603 neisseria u
6	23		318		MTH2_HAEAE	
10	23	100.0	355		PYRH_BRIIME	28ye62 brumella me
11	53	100.0	322	r 4	PYRB_XYLFA	
12	23		323		PYRB_RALSO	
13	23		326	-	PYRH_RHILO	Q98m86 rhizobium l
14	23		335	٠.	PYPR_CAMOR	
15	23		334		PYRB_PSEAE	
16			334	_	PYRR_PSEPU	Q59711 pseudomonas
17			383		YJIM_ECOLI	P39384 escherichia
18			403	e4	FLGE_HELMU	P50611 helicobarte
19	23		503	_	PUR1_PASMU	Q916b8 pastcurella
20	23		504	r-1	PUR1_HAEIN	P43854 haemophilus
=======================================	53		580	- 1	EZRI_BCVIN	F31576 bos taurus
C1	e e	100 0	0 0 0	- 4	EZEI_HUMAN	F15311 homo sapies
23	ű.	100 C	u Œ	p	FZF1_MOUSE	P26040 mus musculu
7.7	e ci	100.0	(F)	٠.	VQ <sup>E</sup> ∩_CAPTT	209466 caemorhabdt
55	[2	91.3	569		NUDC_VIBCH	C9kv27 vibrio chol
26	21	91.3	583		LEP4_PSEST	COsel6 pseudomosus
27	21	٠	366	1	ODPB_SCHPO	Q09171 schizosacch
28	21		396	eH	C43A_DROME	Q9v6a9 drosophila
59	21		397	_	GAL1_TREPA	083433 treponema p
30	[4	91.3	429		PUR2_VIHCH	COKYRT VIETIS CHOT
31	Ę.		437	_	FUR2_XYLFA	Q9pc09 xylella fas
32	51	91.3	450	+	YGW9_YEAST	~
33	51	٠. ای	<b>4</b> □		GAPP_PHIME	Q9c3s2 rhitssbium m

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0.417 Mitch. 130.6%, Scote 23: DB 1: Longth 160: Bost Local Similarity 100.0%; Pred. No. 13; Matches 5, Conservative 6, Mismatches 0, Indeis

1 MLPLQ 5

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RESULT 2

Q18192 caenorhabdi P77772 escherichia P32849 saccharomyc Q90469 drosophila Q9W705 xonopus lac F41872 saccharomyc P39846 bacilius su F2051 vaccinia zi G9G11 accopyrum p P33980 caulobacter P3347 escherichia F16162 yersinia pe			оолета.		Fraser C.M., Norris 3.0., Welfastock G.M., White O., Sutton G.G., Osboson R., Gwinn M. Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Attiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Weltch H., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O., Vorfer J.C.	a, the syphilis	This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way mealified and this statement is cut removed. Based by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).	P. CRC64 :
NH31_CABEL RAD5_FEGOLT RAD5_FEGOLT SWS_DROME NCO2_XENLA BN11_YEAST PPS3_BACST PPS3_BACST VAL_VACTV CHEL_AERPE CHEL_CAUCK CHEL_CAUCK	A).IGNMEN'IS	Y656_TREPA SIANDARD; PRI; 160 AA. 084656; 30-MAY-2000 (Rel. 39, Created) MAY-2000 (Rel. 39, Last sequence update) 15-001-2001 (Rel. 40, Last annotation update)	Hypothetical protein TP0650. TP0650. Treponema pallidum. Bacteria: Spirochactales; Spirochactaceae; Treponema NCBL_TaxID-160;	ሌ ሴ ፍ <u>ዋ</u> ጋ ላ ራ	werstock G.M., white Y E.K., Clayton R., F WocLeod M.P., Salzbe Bowell J.K., Chidambe owman C., Cotton M.D. s K., Sandusky M., W.	"Complete garone sequence of Traponama pailidum, the spirochete."; Science 281:375-388(1998).	opyright. It is produce of Bioinformatics a institute. There at tutions as long as it is not removed. Be a dyreement (See http: edisb-sib.ch).	54. 1. 1. 1. 1. 1. Lete proteome. MW; 053796A81A7L898F CRC64;
91.3 583 1 91.3 742 1 91.3 1425 1 91.3 1425 1 91.3 2560 1 91.3 2560 1 87.0 102 1 87.0 102 1		SIANDARD; (Rel. 39, Crea (Rel. 39, Last (Rel. 40, Last	<pre>protein TP065 !!idum. irochaetales; 60;</pre>	M N.A. ols: Pater Pubmodes	Norris S.J., Winn M., Hicke Hardham J.M. Lichardson D., Artiach P., B	77: BELONGS TO	Swiss Institute Swiss Institute Bioinformatic Institute Institutes a licens and It is small to licens and It is to licens	EMBL, AE061239, AAC65623.1; IIGR, TP0650; Interpro, PP00650; Prince PP00130; UPP0054; 1 Prince PP00130; UPP0054; 1 IIGRAMS, TIGRUDAR, UPP0054; 1 FIGHTAMS, TIGRUDAR, UPP0054; 1 FROSTE, PS01306; UPP0054; 1 Hypolhetical protein, Complete pro
33.4 33.5 33.5 33.6 4.4 4.5 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5.0 5	RESULT 1 Y650 TREPA	Y650_TREPA 083656; 30-MAY-2000 30-MAY-2000 16-0:11-2001	Hypothetical TP0650. Treponema pa Bacteria; Sp NCBI_TaxID-1	[1] SEQUENCE FROM N.A. STRAIN-Nichols; MEBLINE-WARFORD.	France Composition of the Compos	"Complete go spirochete" Svience 281:	between the the European use by non modified and entities red	EMBL, AEGGIST TPO65GIST TO 65GIST TPO65GIST TO 65GIST TO 65GIST TO 65GIST TE PROGRAMS. THE PROGRAMS TO 65GIST TO 65GIST TE PROGRAMS TO 65GIST TO 6
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AMAN JU, Shihadawa A., Shibada K., Yoshino M., Itoh M., Ishii Y., Andari J., Shihadawa A., Shibada K., Yoshino M., Itoh M., Ishii Y., Andari J., Shihadawa A., Shibada K., Yoshino M., Adachi J., Fukuda S., Andakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Yamanaka I., Andara K., Izawa M., Nishi F., Eigosawa H., Rondo S., Yamanaka I., Andara T., Andara M., Mashara M., Mashara M., Mashara M., Mashara M., Mashara M., Kochiwa H., Kachiwa H., Kachiwa H., Kachiwa H., Kachiwa I., Andara M., Mashara M., Mashio T., Andari M., Mashara M., Mashio T., Sakai K., Okido T., Futuno M., Andono H., Haldarchi H., Harsh G., Sakai K., Okido T., Futuno M., Andono H., Haldarchi H., Harsh G., Boushatai M.J., Bult C., Fletcher C., Fujia M., Carboldi M., Gustincich S., Hill D., Bojunga N., Carninci P., de Bonaldo M.F., Andono P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Andono P., King H., Kingwald M., Rodrigae T., Shibata Y., Storch K.-F., Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch A., William M., Bull C., Raniya M., Lee N., Mynshaw-Boolis A., Yoshida K., Haseqawa Y., Pawaji H., Kohisaki S., Masaki A., Wasaki A., Wasaki V., Wanaki V., Wanaki V., Wasaki V., Wanaki V., Wanaki
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"Nuclostide sequence of mouse L19 ribosomal protein cDNA isolated in
serrecting with tre oncogene probes.";
NNA Cell Hiol. 9:697-703(1990).
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"High-level expression of the ribosomal protein L19 in human breast.
tumors that overexpress erbB-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                 Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDMAs encoding elongation factor 1 gamma and the ribosomal models 110 %.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank,7PPRT databases
                                                         P14118: P22908;
01 JAN 1990 (Rel. 14, Created)
01 JAN 1990 (Rel. 14, Last sequence update)
15-JUN 2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 20:2598 2598(1992).
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MEDLINE-92285147; PubMcd-1598220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJINE-93185086; PubMed-8095182;
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                                                                                                                                                                                                                60S ribosomal protein 119.
RPL19.
                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                Raffus norvegious (Rat).
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                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECTES-Human;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Hioinformatics and the FMH. outstation the buropean Bioinformatics Institution. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cuttities requires a license apprehent (Suc http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                Chan Y.-L., Lin A., McNally J., Peleq D., Mayuhas O., Wool I.G.; "The primary structure of rat ribosomal protein L19. A determination from the sequence of nucleotides in a cDNA and from the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                     The L19 ribosomal protein gene (RPL19): gene organization,
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; AAP506393P526216 CRC64;
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Viruses, dsDMA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                chromosomal mapping, and novel promoter region.";
Genomics 25:372-380(1995).
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01-DEC-1992 (Rel. 24, Last Sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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Pfam; PF01280; Ribosomal_1.19e; 1.
PROSITE; PS00526; RIBOSOMAL_L19E; 1.
                                                                                                                                                                                              Biol. Chem. 262:1111-1115(1987).
                                                                                                                                                                                                                                                                              SPECIES-Rat; STRAIN-Fischer; MEDLINE=95309903; PubMed=7789970;
                                                     MEDLINE-87109220; PubMed-3542997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S56985; AAB25672.1; -.
EMBL; BC000530; AAH00530.1; -.
EMBL; BC013016; AAH13016.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AK010440; BAH26941.1; --
EMBL, BC010710; AMHUV10.1; --
EMBL, JO2660; AA42071.1; --
EMBL, X92202; CAA57685.1; --
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                                                                                                                                                                      amino acids in the protein.
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PIR, A48992, A48992.
Genew: HGNC:10312; RPL19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S09560; R5RT19.
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8 OR 82.
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                                                                                                                                                                                                    This SWISS-PROT entry is copyright It is produced through a collaboration between the Swiss Institute of Micinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tellord E.A.R., Watson M. S. Morride K., Pavison A.T.;
The DNA sequence of equine herpesvirus-1.";
Virology 189-304-316(1992)
-1- SIMILARITY - RELONGS TO FAMILY THAT GROUPS TOOPTHER HSV-1 (H.51).
                                                                                          simplex virus type 1 tequment protein, and qp10, a qlycoprotein of equine herpesvirus 1 and 4 ";
                                                                           "Antigenic and protein sequence homology between VP13/14, a herpes
                                                                                                                               J. Virol. 65-2320-2326(1001)
-!- SIMILARITY: BELONGS TO FAMILY THAT CROUPS TOCKTHEP HSV-1 (1151)
                                      Whittaker G.R., Riggio M.P., Halliburton I.W., Killington R.A.,
Allen G.P., Meredith D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c 
                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 23, DB 1, Length 244, 100 0%; Pred No 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses, dSDNA viruses, no BNA stage; Herpesviridae:
Alphaherpesvirinae; Varicellovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               c.
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01-DEC-1992 (Pel. 24, Last sequence update)
01-DEC-1992 (Ref. 24, Last annotation update)
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                     MEDLINE-91202570; PubMed=1850013;
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Tellord E.A.R., Watson M.S. MoRr
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SEQUENCE FROM N.A.
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Among Marine E. Janden E. 18 Baker S. Basham D., Stewart A., Radan S. Sequence J. Peat N., Hayles T., Baker S., Basham D., Bowman S., Radarden E., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor K., Cronin A., Davis P., Fertwell T., Fraser A., Contles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Radarder S., Honsey P., McDead S., McDead J., Annes E., Tones L., Tones M., Laalher S., McDead S., McDead J., McDead J., McDead J., McDead J., McDear J., McDead J., McDear J., McDear J., McDead J., McDear J., McDea
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                                                                                 15.JUN-2002 (Rel. 41, Created)
15.JUN-2002 (Rel. 41, Last Sequence update)
15.JUN-2002 (Rel. 41, Last Sequence update)
Serine/throomino-protoin Finase pefi (BC 2.7.1.37) (Cyclin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein. -! SUBUNIT: Interacts with the past cyclin. -! SIMILARIT: BELGINGS TO THE SEKZTHE FAMILE OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A pcl-like cyclin activates the Ros2p-Cdc10p cell cycle 'start' transcriptional factor complex in lission yeast."; Mol. Biol. Cell lli2845-2862(2000).
                                                                                                                                                                                                                                                                             Edkaryota: Fungi; Ascompoda; Schizosaccharomycetes;
Schizosaccharomycetaies, Schizosaccharomycetaceae;
                               288 AA
                                                                                                                                                                                                                                                Schizusacchiromyces pembe (Fission yeast).
                               PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=21848401; PubMed-11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE-20437747; PubMed+10982385;
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                                                                                                                                                                                               kinase pefl) (PHO85 homolog).
                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDC2/CDKX SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lanaka Kili Okayana Hili
                                                                                                                                                                                                                                                                                                                                       Schrizosaccharomyces.
                                                                                                                                                                                                                         PEFI OR SPONING4.11.
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                            PEFL_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN 972
PEF1_SCHPO
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InterPro: IPP002290; Ser\_thr\_pkinase

InterPro; IPR000719; Euk\_pkinase.

EMBL; AB045127; BAB16402.1; -.

HSSP; P24941; 1CKP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21608551; PubMed-11743194;
Goodner B., Hinkle G., Gatting S., Miller N., Blanchard M.,
Ourrollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., lartehouk O., Hpp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz H.,
Falanayan C., Crowell C., Gurson J., Lomo C., Saar C., Strub G.,
Cielo C., Slater S.;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 23; DB 1; Length 288; 100.0%; Pred, No. 25;
                                                                                                                                                                                                      Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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15-JUN-2002 (Ref. 41, Last annotation update)
Aspartate carbamojitransferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7A3077D33F40A8FA CRC54;
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FATHWAY: Pyrimidiue biosynthesis: second step.
SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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ATP (BY SIMILARITY).
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                                                                                      PROSITE; PSOOTO7; PROFEEN KINASE ATP; 1.
PROSITE: PSOOTO8; PROFEIN_KINASE_POM; 1.
PROSITE; PSOOTO8; PROFEIN_KINASE_ST; 1.
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Pfam; PF00069; pkindsc; 1.
ProDom; PD000001; Euk_pkindsc; 1.
SMAKT; SMO0220; S_TKc; 1.
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PYRB OR ATHI308 OR AGR_C_2407.
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between the Swiss Institute of Bioinformatics and the EMBL outstation
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-i- CAIALYIIC ACTIVITY: Carbamoyl phosphate ' L-aspartate - phosphate
                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Beisard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godie T. Goffeau A., Rahn D., Kiss E., Lelaure V., Masuy D., Fohl T., Forteteile D., Puchler A., Purnelle B., Ransperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Gallibert F., Sanalysis of the chromosome sequence of the lequme symbiont Sinorbizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium meliloti (Siborhizobium meliloti).
Bacteria, Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                100.0%; Score 23; DH 1; Length 313; 100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 1; Length 313; Pred, No. 27;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                            Transferase, Complete proteome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrimidine biosynthesis, Transferase, Complete profeome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamoyitransferase (RC 2.1.3.2) (Aspartate
                                                                                                                                                                                                          34055 MW; CA8BCB1948923BD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + N-carbamoyl-L-aspartate.
-!- PATHWAY: Pyrimidine biosynthesis; second step.
-!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6E37984CBB5A6A54 CRC64;
                the Buropean Bioinformaties Institute. Then use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 AA
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                              EMBL: AE008058: AAR87099.1; ALT_INIT.
PROSITE: PS00097; CARBAMOYLTKANSFERASE: 1.
Fyrimidine biosynthesis, Transferase; Como
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS: TIGRO0670; asp_carb_tr; 1, PROSITE; PSO0097; CARBAMOYLIRANSFERASE; 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002029; Asp/orn_cotrant.
InterPro; IPR002082; Asp_carbmltranst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21396507; PubMed-11481430;
                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34025 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: ALS91786; CAC45883,1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                  EMBL; AE009092; AAL42314.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcarbamylase) (AlCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02729; OTCACC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRB OR R01304 OR SMC01360
                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flam; PF00185; ofCace;
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                          313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_Tax1D-382;
                                                                                                                                                                                                                                                                                                                                                            222 MI.RI.Q 226
                                                                                                                                                                                                                                                                                                                          1 MI.RI.Q 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-1021
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                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRH_RHIME
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULI 7
                                                                                                                                                                                                                                                                      Best
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                                                                                                                                                                                                                                                Stein D.C., Gunn J.S., Piekarowicz A., "Sequence similarities between the genes encoding the 3.Ngol and Hacii restriction/modification systems.", Biol. Chem. 379:576-578(198).
-i- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gars
                                                                                                                                                                                     Proteobacteria, beta subdivision, Neisseriaggae, Neisseria
                                                                                                                                                                                                                                                                                                  ROCKEY, CAUSES SPECIFIC METHYLATION ON C-7 ON MOTH SIFANIS, AND PROTECTS THE DNA FROM CLEAVAGE BY THE NGOB! ENDONUCLEASE.

-1- CATALYTIC ACTIVITY: S adenosy! Limothioning + DNA cytosine = S-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        c:
                                                                                                             16-0CT-2001 (kcl. 40, Last sequence update)
16-0CT-2001 (kcl. 40, Last annotation update)
Modification methylase NgOBT (EC 2.1.1.73) (cytosino specific
NGOBIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Pel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Modification methylase Bacil (DC 2.1.1.73) (Cytosine specific
                                                                                                                                                                                                                                                                                                                                adenosyl-L-homocysteine + DNA 5-methylcytosine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 0%: Score 23; DB 1; Length 317.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F0544A525901A414 CRC54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA.
                                                                                           317 AA.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT,
                                                                                           PRI;
                                                                                                                                                                                                                                      MEDLINE-98290322, PubMed-9628358,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00145; DNA_methylase; 1.
PRINTS; PR00105. CSMPTTPPBASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPPO01525; C5_DNA_meth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 AA; 35944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                FMRI: 1142459; AARO3206 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100
Matches 5; Conservative
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD,
                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P05102; 6MHT.
REBASE; 3607; M.NGOBI.
                                                                                                                                                                           Neisseria denerrheeae
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                               NCB1_Tax1D-485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 MLRLQ 260
                                       222 MLRIQ 226
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                   1 MLRLQ 5
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030868;
                                                                                          MTB1_NEIGO
                                                                                                                                                                                      Hacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPOORNOR
                                                                                                    059603;
                                                                               MTB1_NEIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTH2_HANAH
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                       RESULT 8
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the biological forformatics institute. There are no restrictions on its use by non-profit institutions in its sold its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                   MEDLINE 98293322; FubMed-9628358;
Stein D.C., Gunn J.S., Plekarowicz A.;
"Sequence similarities between the genes encoding the S.Ngol and Hacli
restriction/modification systems.";
Hiol. Chem. 379:555-578(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sikain-löm / Arct 23456 / Biotype 1; MEDLNB-20020109; PubMed-1175668; DelVecchio V.G., Kapatral V., Rečkar R.J., Patra G., Mujer C., Los T., Ivatora N., Anberson I., Phostfachary, a A., Lykidis A., Redrih S., Lablorski I., Arsen N., Pisoura M., Bernal A., Manar M., Sutsman E., Svikov E., Elser P.B., Hagius S., OʻCallaghan D., Letesson J.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       -: FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE REGISCY, CANSES SPECIFIC METHYLATION ON C-? ON BOTH STRANDS, AND PROTECTS THE DNA FROM CLEAPAGE BY THE HABLI ENDOUNDLEASE.

| CALLATTIC ACTIVITY: S addrosyl-L.Facthichine. DNA cytosine = S-addrosyl-L.Addrocysterine. Functional Construction of Strands Strands Strands Strands Construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Batteria, Protesharteria, alpha subdivision, Mizobiaceae qroup;
Brucellaceae; Brucella.
                                                                                         Bacteria, Proteobacteria, qamma subdivision, Pasteurellaceae;
Haemophilus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 0%; Score 23; DB 1; Length 318; 150.0%; Ptcd. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002 (Mel. 41, Greated)
15-JUN-2002 (Mel. 41, Last sequence update)
15-JUN-2002 (Pel. 41, Last annotation update)
Asfartule calbasoyltiansterase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Methyltransferase; Restriction system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT:
nethyltransferase HaeII) (M.HaeII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterFro, IPRO01525: C5_DNA_meth.
Pfam: PF00145: DNA_methylase: 1.
PRINTS: PR00105: C5METIRFPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGREAMS, TIGRO0675, dcm, 1, PROSTIE: PS00094, C5_MTASE_1; 1, PROSTIE: PS00095, C5_MIASE_2; 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: AF019754; AA870829.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41# AA; 4567U MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transcarbamylase) (ATCase).
PYRB OR BMEI10670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P05102; 6MHT.
E; 3409; M.Haell.
                                                           Haemophilus aegyptius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brucella melitensis.
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                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-AICC 11116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHOUENCE FROM N.A
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                          HAELIM OR DOMA.
                                                                                                                                                         NCB1_Tax10-725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 MLRLQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLRLQ 5
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simpson A.J.G., Reinards F.D., Arruda P., Abreu F.A., Accencio M., Alvarenda R., Alves L.M.C., Arrya J.E., Baia G.S., Baplista C.S., Alvarenda R., Alves L.M.C., Arrya J.E., Baia G.S., Baplista C.S., Barros M.B., Gomardo A.A., Cardin S., Rove I.M., Brioges M.E.S., Buerto M.R.P., Camardo A.A., Cardin S., Roya J.E., Garraro D.M., Carrer B., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Nero C.M., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Nero C.M., Contino L.D., Cristofani M., Dias-Neto G., Docena C., Bi-Dorry H., Frada J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Administra M., Colombo C., Lambais M.R., Littajina J.P., Hopelsel J.D., Junquelra M.C., Remper E.L., Kitajina J.P., A. Ho P.L., Hohelsel J.D., Junquelra M.E., Lambais M.R., Leite L.C.C., A. Arricer J.E., Kuramae E.E., Laignett F., Lambais M.R., Leite L.C.C., A. Marchado M.A., Madeira A.M.H.N., Madlins E.M.F., Matsukuma A.Y., Marchas B.C., Miyaki C.Y., Montelto L.E.S., Monto D.H., Nadai M.A., Nascimento A.L.T.O., Netto L.E.S., Nibani A. J., Nobrega P.G., Vinoreita M.A., Paris A.,
                                                              Proc. Nail. Acad. Sci. U.S.A. 99-443-448(2002)
-i- CATALYTIC ACTIVITY: Garbamoyl phosphate + L-aspartate - phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sdeb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Proc. Natl. N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%, score 23; PR 1; Longth 322; 100.0%; Pred. No. 28; 0; Indots ive 0; Mismatches 0; Indots
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSTE; PSO0097; CARRAMOYLTRANSFERASE; 1.
Pyrimidine biosynthesis, Transferase, Complete protecume.
SEQUENCE 322 AA; 34802 MR; 8186208851895218 CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 JUN-2002 (Rel. 41, Last segmence update)
15 JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamoyllranslerase (EC 2.1.3.2) (Aspartate
                                                                                                              -1- PATHWAY: Pyrimidine biosynthesis; second step.
-1. SIMILARITY: HELONGS TO THE ATCASES/CTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatchos
                                                                                                                                                                                                                                                                                                                                         TPR002082: Asp_carbmltransf.
                                                                                                                                                                                                                                                                                                                       InterPro; IPR002024 - Asp,Zorn_Cotranf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPT;
                                                                                                                                                                                                                                                                                                                                                                                                         HIGKFAMS; HIGRO0670; asp_carb_tr; 1
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    N-carbamoyl-L-aspartate,

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                                                                                                                                                                                                                                                                                                       EMBL; AE009702; AAL53912.1; -.
                                                                                                                                                                                                                                                                                                                                                                       Plam; PE02729; Ofcace_M, 1.
PRINTS: PRODION: AUTCASE
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cs 5: Conservative
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                                                                                                                                                                                                                                                                                                                                                       Plam; PF00185; ofcace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa.
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                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
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Protxoto B.R., Pereira G.A.G., Pereira H.A. Ji., Pesquero J.H., Ouaggio R.B., Roberto P.G., Rodriques V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., a Silva A.C.E., da Silva F.R., Silva F.R., Silva R. B. Jr., Silva R. B. Jr., Silva R.B., Truff D., Tsai S.M., Isuhako M.H., Vallada H., Van Sluys M.A., Verjovski Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C., Schula Istidiosa.";
                                                                                                                                                                                                                                                                                              + N-carbamoyl-L-aspartate.
-!- PATHWAY: Pyrimidine biosynthesis, second step.
-!- SUBUNIT: CONFAINS SIX CATALYTIC AND SIX REGULATORY CHAINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salanoubat M., Genin S., Artiquenave F., Gouzy J., Mangenot S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria: Protecharteria, beta subdivision: Palstonia group:
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100.0%; Pred. No. 28;
Live 0, Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGROD670; asp_carb_Lr; 1.
PROSTRE; PSRONGY: CARRAWOLTERANSE: 1.
FY.Emidine biosynthesis; Tidinsterase: Complete profeome.
SKOURNCE 322 As; 34637 MM; DIDDESCC4F5A7EAD CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbameritransferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                               SIMILAPITY).
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InterFro, IPR002082, Asp_carbmltrans1
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                                                                                                                                                                                                                                            Nature 406:151-159(2000).
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InterPro; IPR002082; Asp_carbmltransf
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                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration deckeen the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics last the are to restrictions on its use, by non-piefit institutions as long as its content is in no way
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                                                                                                                                                                                                                                        use by moneporfit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish.sh.ch/announce/
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CAIALYIIC ACIIVIIY: Carbamoyl phosphate + L-aspartate - phosphate
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Phyllobacteriaceae; Mesochlichium
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aspartate carbamoyltranslerase (EC 2.1.3.2) (Aspartate
              PATHWAY: Pyrimidine biosynthesis; second step.
SIMILARITY: BELOWS TO THE ATCASES/OTCASES FAMILY.
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PROSITE; PSO0097; CARBAMOYITRANSFERASE; 1.
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InterPro: IPR002029; Asp.com Cofranf
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    N-carbamoy1-1.-aspartate.

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Matches 5; Conserva
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or send an email to license@lsb-sib.ch).
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Fiscen J., Heldeberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Fotocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smil J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan A., Emasar G.M.; Complete genome sequence of Caulobacter crescentus.; "Complete genome sequence of Caulobacter crescentus."; Fig. Natl. Acid. Sci. S. A., 94 414 (444) (2011)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             !- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                               :.
O
                                                                                                                                                                                                                                                                     lud.u%; Score 23; DB 1; Length 326; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1, Length 332;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                           PROSTIE: PS00097; CARBAMOTITRANSFERASH; 1.
Pyrimidine biosynthesis; Transferase; Complete proteome.
Stocknot: 316 AA; 35212 MW, E75Ab130059930F5 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGROUGTO; asp_carb_tr; 1.
PROSTE; PSOUGT; CARHAMOVIRANSERRASE; 1.
PYLINIGINE INSOUGHS: Transferase, Complete profeome.
SEQUENCE 332 AA; 35509 MW; 13261CC5C13E1AE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 JUN-2002 (kei. 41, Last sequence update)
15 JUN-2002 (kei. 41, Last annotation update)
Aspartate carbamogitzansferase (kC 2.1.3.2) (Aspartate

    PATHWAY: Pyrimidine biosynthesis; second step.
    SIMILARITY: BELONGS TO THE AICASES/OTCASES FAMILY.

                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPP002082; Asp_carbmltransf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002029; Asp/Orn_Cotranf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPT;
                                                                                                      11GREAMS; IIGRUÕŠ70; asp_carb_tr; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE005913; AAK24414.1; -. HSSP; P00479; BCSU.

    N-carbamoyl-L-aspartate.

Pfan, PF00185, OrCace, 1.
Pfam, PF02729, OrCace_N, 1.
PRINTS: PF00100, AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pram; PF02/29; OTCase_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcarbamylase) (ATCase).
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-AIGC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINIS; PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDAPD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piam; PF00185; Ofcace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caulobacter crescentus.
                                                                                                                                                                                                                                  query Match
Best Local Similarity
5, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Rost (chal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCB1_Tax1D=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRB OR CC2443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 MERIO 232
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or send an email to licensealsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN AICC 18692 / PAG1;
MEDLINE-20437347: PLUMECT10944043;
Stover C.K., Pham X.-U.F., Erwin A.L., Mizoguchi S.D., Warrener P.,
Bickey M.J., Brinkman F.S.L., Hulnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Radman S., Yuan Y.,
Brody L.L., Goltry L., Tolentino E., Westbrock-Radman S., Yuan Y.,
Brody L.L., Goltry L., Folder K.P., Fas A., Larbiq K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen L.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAG1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406:959-964(2000).
      Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i N carbamoyl-L aspartate.
PATHWAY: Pyrimidine biosynthesis; second step.
SUHUNIT: HETEKODODECAMER OF 6 ACTIVE PYRB SUBUNIIS AND 6 NON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN AICC 15692 / PAOL;
Vicktey J.F., Schutt M.J., Benjamin R.C., Cunin R., Shanley M.S.
    ÷
                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 23; DB 1; Length 334; 100.0%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrimidine biosynthesis, Transferase, Complete proteome.
CONFLICE 206 206 R -> A (IN REF. 1).
SEQUENCE 334 AA; 36629 MW; 2DC90450FA2E42E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                      16 oct-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Asparlate carbamoyltranslerase (EC 2.1.3.2) (Asparlate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC PYRC' SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                  334 AA.
  Mismatchos
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PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO02082; Asp_carbmitransf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002029; AspZorn_Cotrant.
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                     01-Nov 1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 1.19649; AAA25976.1; -.
EMBL; AE004477; AAG03791.1;
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                                                                                                                                                                                                                                                                                                    transcarbamylase) (ATCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
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5; Conservative
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00185; OTCace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00479; 3CSU.
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                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-287;
                                                                              241 MLRLQ 245
                                                                                                                                                                                                                                                                                                                     PYRB OR PA0402
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                                       1 MI.RI.Q 5
                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas.
                                                                                                                                                                                PYRB_PSEAE
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                                                                                                                                                             PYRB_PSEAE
  Matches
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Caps

0;

0; Indels

0; Mismatches

Best Local Similarity 100,0 Matches 5, Conservative

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237 MLRLQ 241
1 MI.RI.Q 5
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Search completed: January 16, 2003, 16:51:16 Job time . 9.28571 secs